Remarks

Reconsideration of this Application is respectfully requested. Claims 3 and 47-50 are pending in the application, with claims 3 and 47-50 being the independent claims. Claims 3 and 47-50 are pending and under consideration. Under 37 C.F.R. § 1.116(b), claims 47-50 have been amended to place them in better form for allowance or appeal. Support for these amendments may be found, *inter alia*, in the specification as-filed at paragraphs [0003], [0005], [0009], [0017], [0022-0025], [0028], [0032], [0033], [0036], [0037], [0042], [0049], [0060-0064], [0068], [0069], Examples 1-7 [0073-0087], Examples 8-11 [0090-0102] and Table 1. These changes are believed to introduce no new matter, and their entry is respectfully requested. Claims 51-70 have been withdrawn by the Examiner as allegedly being directed to a non-elected invention.

Based on the following remarks, Applicants respectfully request that the Examiner reconsider all outstanding objections and rejections and that they be withdrawn.

Election/Restriction

The Examiner has withdrawn newly-presented claims 51-70 as allegedly being directed to a distinct invention from the compositions recited in claims 3 and 47-50. (Office Action of 10/26/2006, hereinafter "OA", at page 2.) The Examiner asserts that "[s]ince applicant has received an action on the merits for the originally presented invention, this invention has been constructively elected by original presentation of prosecution on the merits," citing MPEP § 821.03. (See Id.) Applicants respectfully traverse the withdrawal of claims 51-70.

A. Claims 54, 58, 62, 66 and 70

Applicants respectfully assert that claims 54, 58, 62, 66 and 70 should be rejoined with the claims under consideration in the present application because they depend from either allowable claim 3 or claims 47-50, which are also believed by Applicants to be in condition for allowance. (*See* pages 12-19, *infra*). Presently-withdrawn claims 54, 58, 62, 66 and 70 are directed to a method for producing a polypeptide using the nucleic acid sequences recited in claims 3 and 47-50 (*i.e.*, the nucleic acid sequence of SEQ ID NO: 115 and sequences having 95%, 90%, 85% or 83% identity with SEQ ID NO:115). The USPTO published a Notice in the March 26, 1996 Official Gazette setting forth the guidelines for the treatment of product and process claims in light of the Federal Circuit's decisions in *In re Ochiai*, 71 F.3d 1565 (Fed. Cir. 1995), and *In re Brouwer*, 77 F.3d 422 (Fed. Cir. 1996). *See* 1184 OG 86 (March 26, 1996). Specifically, the Notice states that in the case of an elected product claim, rejoinder will be permitted when a product claim is found allowable and the withdrawn process claim depends from or otherwise includes all the limitations of an allowed product claim. *See Id*.

In the present case, the Examiner has essentially restricted between the product recited in claims 3 and 47-50, and methods of using the product, as recited in claims 54, 58, 62, 66 and 70. In the Office Action dated October 24, 2006, the Examiner stated that claim 3 is allowable because "the prior art does not describe an isolated nucleic acid comprising SEQ ID NO:115." (OA at page 4). Although the Examiner has rejected claims 47-50 under 35 U.S.C. §112, first paragraph, Applicants believe this rejection will be overcome, and that presently-pending claims 47-50 are in condition for allowance.

(See pages 12-19, infra). Thus, in view of the guidelines set forth in the March 26, 1996 Atty. Dkt. No. 2399.0070001/JAG/LAV

Official Gazette Notice, as well as the Federal Circuit's decisions in In re Ochiai and In re Brouwer, Applicants respectfully request reconsideration and rejoinder of withdrawn method claims 54, 58, 62, 66 and 70 with presently-pending product claims 3 and 47-50.

В. Claims 51-53, 55-57, 59-61, 63-65 and 67-69

The Examiner has also withdrawn claims 51-53, 55-57, 59-61, 63-65 and 67-69 from consideration, asserting that they are directed to distinct compositions "such as a genetically engineered host cell, comprising a recombinant vector comprising a distinct polynucleotide sequence." (OA at page 2.) Applicants respectfully traverse this restriction.

(i) **Claims 51-53**

Claims 51-53 should be rejoined and fully examined for patentability in accordance with 37 CFR §1.104 because they were presented for examination prior to final rejection or allowance, and require all the limitations of allowable claim 3. See MPEP §821.04(a). Claims 51-53 depend directly or indirectly from claim 3, and are directed to compositions requiring the allowable product of claim 3 (SEQ ID NO: 115). In the Office Action of October 24, 2006, the Examiner essentially restricted claims 51-53 from the present application by withdrawing them as allegedly being directed to a non-elected invention. (OA at page 2). Applicants respectfully traverse this restriction.

Section 821.04(a) of the MPEP states that an amendment presenting additional claims that depend from, or otherwise require all the limitations of, an allowable claim will be entered as a matter of right if the amendment is presented prior to final rejection or allowance, whichever is earlier. See MPEP 821.04(a). In this case, the additional claims presented in the September 13, 2006 Amendment and Reply (including claims 51-Atty. Dkt. No. 2399.0070001/JAG/LAV

53) were submitted before a final rejection was issued. Additionally, the Examiner has indicated that claim 3, directed to the nucleic acid sequence of SEQ ID NO:115, is allowable. (See OA, page 4). Claims 51-53 depend directly or indirectly from claim 3, and recite compositions requiring the allowable product of claim 3 (SEQ ID NO: 115). Furthermore, claim 3 is a generic linking claim with regard to claims 51-53. See MPEP §809. When all claims directed to the elected invention are allowable, should any linking claim be allowable, the restriction requirement between the linked inventions must be withdrawn. See MPEP §809. Any claims directed to the nonelected invention(s), previously withdrawn from consideration, and which depend from or require all the limitations of the allowable linking claim must be rejoined and will be fully examined for patentability. See MPEP §809. Thus, according to MPEP §§ 809 and 821.04(a), at least claims 51-53, all of which depend directly or indirectly from allowable claim 3 should have been considered in the Office Action of October 24, 2006. Accordingly, Applicants respectfully assert that claims 51-53 should be rejoined with the presently-pending claims and fully examined for patentability in accordance with 37 CFR §1.104.

(ii) Claims 55-57, 59-61, 63-65 and 67-69

Claims 55-57, 59-61, 63-65 and 67-69 should be rejoined and fully examined for patentability in accordance with 37 CFR §1.104 because they depend directly or indirectly from claims 47-50, and although the Examiner has rejected independent claims 47-50 under 35 U.S.C. §112, first paragraph, this rejection is believed to have been overcome, putting claims 47-50 in condition for allowance. *See* MPEP §821.04(a). Claims 55-57, 59-61, 63-65 and 67-69 are directed to compositions such as recombinant Atty. Dkt. No. 2399.0070001/JAG/LAV

vectors and genetically engineered host cells, requiring either the allowable product of claim 3 (SEQ ID NO: 115), or sequences that have 95%, 90%, 85% or 83% identity with SEQ ID NO: 115. In the Office Action of October 24, 2006, the Examiner essentially restricted claims 55-57, 59-61, 63-65 and 67-69 from the present application by withdrawing them as being allegedly directed to a non-elected invention. (OA at page 2). Applicants respectfully traverse this restriction.

Section 821.04(a) of the MPEP states that when restriction has been required between independent or distinct products, or between independent or distinct processes, and all claims directed to an elected invention are allowable, any restriction requirement between the elected invention and any nonelected invention that depends from or otherwise requires all the limitations of an allowable claim should be withdrawn. See MPEP §821.04(a). In this case, although genetically engineered host cells and recombinant vector could technically be classified into a different class and subclass, the search for SEQ ID NO:115 or sequences having 95%, 90%, 85% or 83% identity with SEQ ID NO: 115 would be coextensive with the different classes comprising host cells and recombinant vectors. As noted above, the Examiner stated in the Office Action of October 24, 2006, that SEQ ID NO: 115 is found to be free of the prior art. (OA, page 4). Thus, any composition that includes SEQ ID NO: 115 and is not a product of nature will also be free of the prior art. Furthermore, Applicants assert that examination of claims 55-57, 59-61, 63-65 and 67-69 would not impose a burden on the examiner because the examiner has not established that the search for SEQ ID NO:115 would not have provided results pertinent to these claims. See MPEP §808.02. Accordingly, since claims 55-57, 59-61, 63-65 and 67-69 are directed to compositions encompassing an Atty. Dkt. No. 2399.0070001/JAG/LAV allowable product, Applicants respectfully request that they be rejoined and fully examined for patentability in accordance with 37 CFR §1.104.

Rejections under 35 U.S.C. § 112, first paragraph

A. Claims 47-50 do not contain new matter

The Examiner has rejected claims 47-50 under 35 U.S.C. § 112, first paragraph, asserting that the amendments of September 13, 2006, introduce new matter that was not described in the specification in such a way as to reasonably convey to one skilled in the art to that the inventor had possession of the inventions as now claimed. (OA at page 3.) Applicants respectfully traverse this rejection.

The specification and claims, as originally filed, provide proper descriptive support for the amendments of September 13, 2006, including the subject matter of claims 47-50. Presently-pending claims 47-50 are directed to an isolated polynucleotide comprising a nucleic acid sequence from 83-100% identical to the sequence of SEQ ID NO: 115, wherein the isolated polynucleotide encodes a toxin capable of binding to a sodium channel.

Written description does not require that the subject matter of the claim need be described literally, *i.e.*, using the same terms or *in haec verba*, in order for the disclosure to satisfy the description requirement. If a skilled artisan would have understood the inventor to be in possession of the claimed invention at the time of filing, even if every nuance of the claims is not explicitly described in the specification, then the adequate description requirement is met. *See, e.g., Vas-Cath, Inc. v Mahurkar*, 935 F.2d 1555 at 1563 (Fed. Cir. 1991); *Martin v. Johnson*, 454 F.2d 746, 751(CCPA 1972) (stating "the

description need not be in *ipsis verbis* [i.e., "in the same words"] to be sufficient"); see also MPEP §2163.

Additionally, the "Methodology for Determining Adequacy of Written

Description" found at section 2163.II.A.2. of the MPEP provides that, prior to

determining whether the disclosure satisfies the written description requirement for the

claimed subject matter, an Examiner should review the claims and the *entire*specification, including the specific embodiments, figures, and sequence listings, to

understand how the Applicant provides support for the various features of the claimed
invention.

In this case, a skilled artisan would have understood the inventor to be in possession of the claimed invention based on the disclosure in the specification and sequence listing as originally filed, which provide descriptive support for the nucleic acid sequences that are at least 95%, 90%, 85% and 83% identical to SEQ ID NO:115. For example, Table 1, column D, on page 3 of the specification discloses a list of 71 nucleic acid sequences¹ that encode isolated scorpion toxins. (specification at page 3). Table 1 and the sequence listing are part of the specification, and should be considered when evaluating the adequacy of the written description.

¹ These sequences also appear in the sequence listing as originally filed.

	SEQ ID		SEQ ID	
<u>Species</u>	nucleic acid	% identity with	primary protein	% identity with
	coding region of	SEQ ID 115	structure of mature	SEQ ID 116
	mature toxin		<u>toxin</u>	
C. exilicauda	43	86.5 %	44	75%
C. exilicauda	47	87 %	48	76.5%
C. nocius	91	87.7%	92	74.2%
C. elegans	111	82.8%	112	73.3%
C. elegans	115	100%	116	100%
C. elegans	119	99.5%	120	95.3%
C. sculpturatus	151	88.5%	152	79.6%
C. sculpturatus	195	88%	196	76.5%

The sequences in the above table are those sequences that share the closest homology with SEQ ID NO:115 as determined by Examiner Desai's sequence search.

(See Appendix A, attached hereto). The percent homology that each molecule listed in Table 1 has with SEQ ID NO:115 is an inherent feature of each sequence described in the specification. The percent homology between the sequences is a fact based on the structure of the sequences disclosed in the specification and sequence listing. The determination of percent identity between nucleic acid sequences was within the skill of the ordinary artisan as of the filing date of this application.

The sequences listed in the above table are part of the specification as-filed. As shown in the above table, SEQ ID NOs: 43, 47, 91, 111, 119, 151, and 195 share 86.5%, 87%, 87.7%, 82.8%, 99.5%, 88.5%, and 88% sequence identity with SEQ ID NO:115, respectively. Applicants assert that the specification as-filed, including the sequence listing, would have reasonably conveyed to one skilled in the relevant art that the inventors had possession of the claimed nucleic acid sequences having 95%, 90%, 85% or 83% identity with SEQ ID NO:115 at the time the application was filed. Therefore,

the specification provides adequate written description under 35 U.S.C. §112, first paragraph, for a range of sequences which possess from 83% to 100% sequence similarity with SEQ ID NO:115, as recited in claims 47-50. Accordingly, this rejection is believed to have been overcome. Reconsideration and withdrawal of the New Matter rejection of claims 47-50 is respectfully requested.

В. The specification provides proper written descriptive support for claims 47-50

The Examiner has rejected claims 47-50 under 35 U.S.C. § 112, first paragraph, as failing to comply with the written description requirement. More specifically, the Examiner asserts that the recited subject matter was not described in "the specification in such a way as to convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention." (OA at pages 3-4). The Examiner also asserts that "[o]ne of skill in the art cannot visualize or recognize which nucleic acid sequences can be modified and/or mutated such that the polynucleotide with reduced percent identity retains the function of a toxin affecting sodium and potassium channel activity as disclosed for SEQ ID NO:115." (OA at pages 3-4). Applicants respectfully traverse this rejection.

The specification as-filed provides adequate written descriptive support for the nucleic acids recited in claims 47-50, because a person of ordinary skill at the time of filing could have visualized or recognized the identity of the members of the recited genus based on recited functional requirements and known structural similarities shared by polynucleotides that are at least 95%, 90%, 85% and 83% identical to SEQ ID NO:115. More specifically, the ordinary artisan reading the specification in conjunction with what was generally known in the art of scorpion toxins would have known that the sequences that are at least 95%, 90%, 85% or 83% identical to SEQ ID NO:115 would need to bind to the Na⁺ channel and possess four cysteine bonds to fall within the scope of claims 47-50.

An objective standard for determining compliance with the written description requirement of 35 U.S.C. §112, first paragraph, is, "does the description clearly allow persons of ordinary skill in the art to recognize that he or she invented what is claimed?" In re Gosteli, 872 F.2d 1008, 1012 (Fed. Cir. 1989), see also MPEP 2163.02. An applicant may show possession of the claimed invention by describing the claimed invention with all of its limitations using such descriptive means as words, structures, figures, diagrams, and formulas that fully set forth the claimed invention. See Lockwood v. American Airlines, Inc., 107 F.3d 1565, 1572 (Fed. Cir. 1997). Moreover, the disclosure of a species has also been found to be sufficient to support a claimed genus when the disclosure of species would lead a person of ordinary skill to the genus. See In re Herschler, 591 F.2d 693 (CCPA 1979); see also MPEP 2163.05.). In Herschler, the Court held that the disclosure of one corticosteroid was sufficient to support "physiologically active steroid" because the use would lead one of ordinary skill to the entire class of compounds. 591 F.2d at 697. The Federal Circuit has held that when generic elements of a claim are so well known and thoroughly characterized in the art that their recitation alone is sufficient to convey distinguishing information regarding their identity, the written description requirement for those elements is fully satisfied. See Amgen Inc. v. Hoechst Marion Roussel Inc., 65 U.S.P.Q.2d 1385, 1398 (Fed. Cir. 2003). Another important consideration in assessing written description of a claimed Atty. Dkt. No. 2399.0070001/JAG/LAV invention is the knowledge of one skilled in the art. See Bilstad v. Wakalopulos, 386 F.3d 1116, 1126 (Fed. Cir. 2004).

(i) The encoded toxins of claims 47-50 must be capable of binding to Na+ channels

In this case, claims 47-50 have been amended to recite an isolated polynucleotide comprising a nucleic acid sequence from 83-100% identical to the sequence of SEQ ID NO: 115, wherein the isolated polynucleotide encodes a toxin capable of binding to a sodium channel. As discussed above, the specification as-filed, including the sequence listing, provides proper written descriptive support under 35 U.S.C. §112, first paragraph, for polynucleotides that are at least 95%, 90%, 85% and 83% identical to SEQ ID NO:115, as recited in claims 47-50. Furthermore, all of the publications cited in the specification have been incorporated by reference in their entirety, and thereby provide additional descriptive support for the presently pending claims. (specification paragraph [0105]).

Applicants explain in the specification that scorpion toxins generally fall into two categories: the long chain toxins, 60-76 amino acids in length, which block the Na⁺ channel in excitable cells; and the short chain toxins, 29-41 amino acids in length that affect K⁺ channels. (specification paragraph [0004]). The claimed toxins are all Na⁺ channel toxins, 60-76 amino acids in length, and they all bind to the membrane bound sodium channel. (specification paragraph [0005]). It is the binding of the toxin to the cation channel (the Na⁺ channel) that causes most of the toxicological symptoms in a patient. (specification paragraph [0009]; *see also*, Dehesa-Davilla, page 225).

The specification describes isolated and purified scorpion toxin nucleic acid sequences in the sequence listing, as well as in Table 1. The ordinary artisan reading the specification in light of what was known in the art would have recognized that the claimed sequences fall into the genus of long chain Na⁺ channel blocking toxins. (See specification paragraph [0004]). Thus, the ordinary artisan as of the filing date would have understood that claims drawn to SEQ ID NO:115 or sequences having 95%, 90%, 85% and 83% sequence identity with SEQ ID NO: 115 are directed to Na⁺ channel blocking toxins.

The encoded toxins of claims 47-50 posses a common (ii) structural motif

The Na⁺ channel toxins from scorpions also possess a common structural motif. Applicants explain in the specification that these Na⁺ channel affecting scorpion toxins posses eight cysteine residues which form four cysteine bonds in the mature toxin. (specification paragraph [0004]; see also Possani et al. at page 290, column 2). The common structural motif consists of one stretch of α helix plus three strands of β sheet in antiparallel arrangement, connected by variable regions forming loops. (specification paragraph [0004]; see also Possani et al. p 287, 290). The cysteine residues are numbered consecutively 1-8 from the N- to the C- terminal of the toxin. Cysteine residues 1 and 8, 2 and 5, 3 and 6, as well as residues 4 and 7 form the four disulfide bridges. These disulfide bonds are conserved in all of the Na⁺ channel blocking scorpion toxins that were known as of the filing date of the presently-pending application, including the sequences disclosed in the specification. (specification paragraph [0004]; see also Possani et al. p 290, column 2; see also APPENDIX B attached hereto, which

shows a sequence alignment of the sodium channel toxins disclosed in the specification, and highlights the conserved cysteine residues). In fact, as of the filing date of the present application, all Na⁺ channel-specific toxins were known to be stabilized by four disulfide bridges. (specification paragraph [0004]; see also Possani et al. p 287). Thus, the ordinary artisan reading the specification in light of what was known in the art would have recognized and understood that the recited sequences having 95%, 90%, 85% and 83% sequence identity with SEQ ID NO: 115 would also possess the conserved structural motif of four cysteine bonds.

Based on the combination of what was known in the art about scorpion toxins at the time of filing and the disclosure of seven species of nucleic acid that fall within the scope of claims 47-50, the specification conveys to one of ordinary skill in the art that the recited polynucleotides fall into the genus of long chain Na⁺ channel-blocking toxins possessing a conserved structural motif of four cysteine bonds.

> The USPTO's Written Description Guidelines (iii) Support a Finding of Proper Written Descriptive Support for **Claims 47-50**

The USPTO's "Revised Interim Written Description Guidelines Training Materials" (hereinafter, "Guidelines") provides 18 examples describing how to determine whether the written description requirement of 35 U.S.C. §112, paragraph 1, is satisfied. The facts set forth in Example 14 are almost identical to the present situation, and support a finding of proper written descriptive support for presently-pending claims 47-50.

First, the language of claims 47-50 is extremely similar in form and substance to that of the sample claim provided in Example 14, which recites:

A protein having SEQ ID NO: 3 and variants thereof that are at least 95% identical to SEQ ID NO: 3 and catalyze the reaction of $A \rightarrow B$.

Guidelines, p. 53. Similarly, claims 47-50 require that the claimed polynucleotide is at least 83% identical to SEQ ID NO:115 (the reference compound) and encodes a toxin that is capable of binding to a sodium channel, which is an essential feature of the claimed invention. Thus, the first requirement of Example 14 is met.

Second, the *Guidelines* state that a search of the prior art indicated that exemplified SEQ ID NO: 3 was novel and unobvious. *Id.* at page 54. In the present case, the Examiner stated in the Office Action of October 24, 2006, that the prior art does not describe an isolated nucleic acid comprising SEQ ID NO: 115, which is recited in claims 47-50. (OA at page 4). Thus, the second requirement set forth in Example 14 has been satisfied with regard to currently pending claims 47-50.

Third, an actual reduction to practice of a single disclosed species was deemed sufficient to support the recited genus of proteins that must be variants of exemplified SEQ ID NO: 3. See Guidelines, p. 54. The Guidelines state that the actual reduction to practice one species was sufficient because all of the variants were required to possess the specific functional activity and had a high percent structural identity with the reference compound. See Guidelines, p. 54. In the present case, Applicants have shown possession of the claimed invention by a reduction to practice as evidenced by the descriptive support for at least seven sequences that fall within the scope of the claims, as well as support for the functional element of the claims. (See specification, Table 1,

and the sequence listing). Thus, the third requirement set forth in Example 14 of the Guidelines has been satisfied.

Fourth, procedures for making variants of exemplified SEQ ID NO:3 which have 95% identity to SEQ ID NO:3 and retain its activity were conventional in the art. See Guidelines, p. 53. In the present case, methods for making variants that are at least 83% identical to the reference compound were known in the art at the time of filing, and are described in our specification. (See Molecular Cloning: A Laboratory Manual (2nd ed.), Sambrook et al. (Cold Spring Harbor Lab. Press, 1989), chapters 15-18; see also specification [0040]). Thus, the fourth requirement set forth in Example 14 of the Guidelines has been satisfied with regard to presently pending claims 47-50.

Fifth, an assay was described in the specification that identified the other proteins having the binding activity recited in the example claim. See Guidelines, p. 53. In the present case, the toxins that are at least 95%, 90%, 85% or 83% identical to SEQ ID NO:115 can easily be tested for their binding to the Na⁺ channel. (specification paragraph [0005]; see also Couraud et al. p10-12.] Although there are many different ways to test the binding of a toxin to a Na⁺ channel, one test described in the specification through an incorporated reference uses a rat synaptosome and a labeled toxin. (specification paragraph [0005]; see also Couraud et al. p10-12). Thus, the fifth requirement set forth in Example 14 of the Guidelines has been satisfied with regard to presently pending claims 47-50.

Based on the requirements set forth in Example 14 of the USPTO's Revised Interim Written Description Guidelines Training Materials, as well as the common structural motifs and functional requirements, the specification conveys to a person of Atty. Dkt. No. 2399.0070001/JAG/LAV ordinary skill in the art that the inventors had possession of, and broadly described, an isolated polynucleotide comprising a nucleic acid sequence from 83-100% identical to SEQ ID NO:155, wherein the isolated polynucleotide encodes a toxin that is capable of binding to a sodium channel. Thus, the specification provides adequate written description under 35 U.S.C. §112, first paragraph, for an isolated polynucleotide as recited in presently-amended independent claims 47-50, as well as those claims which depend therefrom. Accordingly, this rejection is believed to have been overcome. Reconsideration and withdrawal of the rejection of claims 47-50 is respectfully requested.

Conclusion

The Examiner has indicated that claim 3 directed to SEQ ID NO: 115 is allowable.

All of the stated grounds of objection and rejection have been properly traversed, accommodated, or rendered moot. Applicants therefore respectfully request that the Examiner reconsider all presently outstanding objections and rejections and that they be withdrawn. Applicants believe that a full and complete reply has been made to the outstanding Office Action and, as such, the present application is in condition for allowance. If the Examiner believes, for any reason, that personal communication will expedite prosecution of this application, the Examiner is invited to telephone the undersigned at the number provided.

CORONA VILLEGAS *et al.* Appl. No. 10/721,793

Prompt and favorable consideration of this Amendment and Reply is respectfully requested.

Respectfully submitted,

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

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Sequence 115, Application US/10721793

PUBLICATION NO. US2000065331A1

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APPLICANT: Beceril Lujan, Baltazar

APPLICANT: Women: 2099-001001

7 TILE OF INVENTION: Venom of Scorpions of the Genus Centruroides

7 TILE OF INVENTION: Women: US/10/721,793

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COTHER INFORMATION: Product= Sodium-channel modifier toxin
US-10-721-793-115
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US-10-721-793-163
US-10-721-793-163
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US-10-721-793-163
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           FEATURE:
NAME/KEY: CDS
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1: /cgn2_6/prodata//pubpna/USOF PUBCOMB.seq:*

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Copyright (c) 1993 - 2006 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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US-10-721-793-119

US-10-721-793-119

Sequence 119, Application US/10721793

Publication No. US20050065331A1

GENERAL INFORMATION:
APPLICANT: Corona villegas, Miguel
APPLICANT: Garcia Rodriquez, Ma Connuelo
APPLICANT: Garcia Rodriquez, Ma Connuelo
APPLICANT: Garcia Rodriguez, Ma Connuelo
APPLICANT: Garcia Briones, Georgina
APPLICANT: Becernil Lujan, Baltazar
APPLICANT: Becernil Lujan, Baltazar
APPLICANT: Becernil Lujan, Baltazar
APPLICANT: Recombinant Immunogens for the Genus Centruroides
TITLE OP INVENTION: Venom of Scorpions of the Genus Centruroides
FILE REPERBACE: 2009.007001

CURRENT APPLICATION NUMBER: US 60/430,067

PRIOR APLICATION NUMBER: US 60/430,067

PRIOR PLING DATE: 2002-12-02

NUMBER OF SEQ ID NOS: 294

SEQ ID NO 119

SEQ ID NO 119
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APPLICANT: Garcia Redriguez, Ma Consuelo
APPLICANT: Garcia Beriones, Georgina
APPLICANT: Becseril Lujan, Baltazar
APPLICANT: Recombinant Immunogens for the Generation of Antivenoms to the
TITLE OF INVENTION: Recombinant Immunogens for the Genus Centruroides
TITLE OF INVENTION: Value of Scorpions of the Genus Centruroides
FILE REPRENCE: 2099.007001
CURRENT APPLICATION NUMBER: US 60/410,067
PRIOR PILING DATE: 2002-12-02
PRIOR PILING DATE: 2002-12-02
RNUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
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... LOCATION: (1) ... (192)
... OTHER INPORMATION: Product ... Sodium-channel modifier toxin US-10-721-793-119
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TYPE: DNA
ORGANISM: Centruroides elegans
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| Publication Wo. US2005005531A1
| GENERAL INFORMATION: US2005005531A1
| GENERAL INFORMATION: US2005005531A1
| APPLICANT: Corona Villegas, Miguel
| APPLICANT: Corona Villegas, Miguel
| APPLICANT: Garcia Redriguez, Ma Consuelo
| APPLICANT: Garcia Redriguez, Ma Consuelo
| APPLICANT: Garcia Redriguez, Ma Consuelo
| APPLICANT: Becerril Lujan, Baltazar
| APPLICANT: Becerril Lujan, Baltazar
| APPLICANT: Becerril Lujan, Baltazar
| APPLICANT: Recombinant Immunogens for the Generation of Antivenoms to the ITILE OF INVERTION: Vencom of Scorpions of the Genus Centruroides
| TITLE OF INVERTION: Vencom of Scorpions of the Genus Centruroides
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NAME/KEY: CDS

NAME/KEY: CDS

OTHER INFORMATION: Product Sodium-channel modifier toxin precursor

OTHER INFORMATION: In the macure peptide, the last Cys is amidated, and the last Gly
OTHER INFORMATION: and the last 2 basic aminoacids are cut

NAME/KEY: 3'UTR

NOCATION: (269)..(323)

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100.0%; Score 192; DB 9; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.3e-53;
Matches 192; Conservative 0; Mismatches 0; Indels
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NAME/KEY: mat peptide
LOCATION: (65)...()
CATHER INFORMATION: Product = Sodium-channel modifier toxin
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Centruroides elegans
                                                           181 AATAAAAGATGC 192
    181 AATAAAAGATGC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AATAAAAGATGC 192
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OTHER INFORMATION:
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Sequence 149, Application US/10721793
| Sequence 149, Application No. US200500653131A1
| Publication No. US200500653131A1
| GENERAL INFORMATION:
| APPLICANT: Corona Villegas, Miguel
| APPLICANT: Gracia Rodriguez, Ma Consuelo
| APPLICANT: Garcia Rodriguez, Ma Consuelo
| APPLICANT: Gurrola Briones, Georgina
| APPLICANT: Gurrola Briones, Louival Domingos
| APPLICANT: Possani Poscay, Louival Domingos
| APPLICANT: Possani Poscay, Louival Domingos
| TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
| TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
| FILE REFERENCE: 2099,0070001
| CURRENT APPLICATION NUMBER: US/10/721,793
| CURRENT PLING DATE: 2002-11-26
| PRIOR APPLICATION NUMBER: US 60/430,067
| NUMBER OF SEQ IO NOS: 294
| SEQ ID NOS: 294
| SEQ ID NO 199
| ENDING NOS: 294
| SEQ ID NO 199
| ENDING NOS: 294
| SEQ ID NO 199
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LOCATION: (5)..(262)
OTHER INPORVATION: Product= Sodium-channel modifier toxin precursor
OTHER INFORMATION: In the mature peptide, the last Cys is amidated, and the last G1
OTHER INFORMATION: and the last 2 basic aminoscids are cut
DOCATION: (1)...(192)
COTHER INPORMATION: Product= Sodium-channel modifier toxin
COTHER INPORMATION: Product= Sodium-channel modifier toxin
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
TITLE: that recognize Na+-channels
JOURNAL: Toxicon
VOLUME: 19
PAGES: 1893-1898
DATE: 2001-12-01
DATEMARASE BRITXY DATE:
RELEVANT RESIDUES: (1)..(192)
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Best Local Similarity 88.5%; Pred. No. 6.18-42;
Matches 170, Conservative 0; Mismatches 22; Indels 0
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ORGANISM: Centruroides sculpturatus
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NAME/KEY: 819_peptide
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Publication No. USZ005005531A1

GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Corona Villegas, Miguel
APPLICANT: Corona Villegas, Miguel
APPLICANT: Corona Villegas, Miguel
APPLICANT: Garcis Redriguez, Ma Consuelo
APPLICANT: Walder Cruz, Norma Adriana
APPLICANT: Possani Postay, Lourival Domingos
APPLICANT: Possani Postay, Lourival Domingos
TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
CURRENT PLING DATE: 2003-0070001

CURRENT PLING DATE: 2003-11-26
PRIOR PILING DATE: 2003-11-26
PRIOR PLING DATE: 2003-11-26

NUMBER OF SEG ID NOS: 294

COTTAMAR: Patentin version 3.1
                                                                                NAME/KEY: CDS
LOCATION: (5). (265)
OTHER INFORMATION: Product= Sodium-channel modifier toxin precursor
OTHER INFORMATION: Product= Sodium-channel modifier toxin precursor
OTHER INFORMATION: In the mature peptide, the last Cy8 is smidated, and the last C basic aminoscids are cut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 AAAGACGGTTATCTCGTGGACAGACGGCTGCAAATACACTTGCTGGTATATGGGAGAA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AACAAATACTGCAATAGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTATTGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.2%; Score 190.4; DB 9; Length 323; 99.5%; Pred. No. 4.5e-53; Live 0; Mismatches 1; Indele 0
                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)...(4)
OTHER INFORMATION:
PRATURE:
NAME/CRE: mat peptide
LOCATION: (65)...()
OTHER INFORMATION: Product= Sodium-channel modifier toxin
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             PB: DNA
IGANISM: Centruroides elegans
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Best Local Similarity 99.5
Matches 191, Conservative
                                                                                                                                                                                                           PEATURE:
NAME/REY: 3'UTR
LOCATION: (269)..(323)
OTHER INFORMATION:
PEATURE:
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NAME/KEY: 81g_peptide
LOCATION: (5)..(64)
COTHER INFORMATION:
UB-10-721-793-117
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US-10-721-793-193

i Sequence 193, Application US/10721793

j Fublication No. US20050065331A1

j GENERAL INPOWNATION:
    APPLICANT: Corona Villegas Miguel

j APPLICANT: Corona Villegas Miguel

j APPLICANT: Garcia Rodriguez, Ma Consuelo

j APPLICANT: Becerril Lujan, Baltazar

j APPLICANT: Becerril Lujan, Baltazar

j APPLICANT: Recombinant Immunogens for the Generation of Antivenoms to the

j TITLE OP INVENTION: Venom of Scorpions of the Genus Centruroides

j TITLE OP INVENTION: Venom of Scorpions of the Genus Centruroides

j TITLE OP INVENTION: Venom of Scorpions of the Genus Centruroides

j CURRENT APPLICATION NUMBER: US/10/721, 793

j CURRENT PILING DATE: 2003-11-26

j RINGR APPLICATION NUMBER: US 60/430,067

j RINGR PILING DATE: 2003-11-26

j SOPTHARE: Patentin version 3.1

j SEQ ID NO 193

mention and application version 3.1

j LENGTH: 320
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OTHER INFORMATION: Troducts Sodium-channel modifier toxin precursor
OTHER INFORMATION: In the mature peptide, the last Cys is amidated, and the last Gly
OTHER INFORMATION: and the last 2 basic aminoacids are cut
NAME/KEY: 5'Clip
LOCATION: (266)..(320)
AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, B., Zurita, M. & Possani L.D.
TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
TITLE: that recognize Na+-channels
JOURNAL: Toxicon
VOLUME: 39
ISSUE: 18
ISSUE: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23, Indele
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 80.8%; Score 155.2; DB 9; Best Local Similarity 88.0%; Pred. No. 2.1e-41; Matches 169; Conservative 0; Mismatches 23;
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ORGANISM: Centruroides sculpturatus
FEATURE:
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181 AATAAAACATGC 192
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OTHER INFORMATION:
FEATURE:
NAME/KEY: mac_peptide
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Publication No. US2005006331A1

GENERAL INFORMATION:

APPLICANT: Corona Villegas, Miguel

APPLICANT: General Redriguez, Ma Consuelo

APPLICANT: General Enders

APPLICANT: General Lujan, Baltana

APPLICANT: Beceril Lujan, Baltana

APPLICANT: Possani Postey, Lourival Domingos

TITLE OF INVENTION: Vence of Scorpions of the Generation of Antivenoms to the

FILE REPRENSENCE: 2099, 1070001

FILE REPRENSENCE: 2099, 1070001

CURRENT PILING DATE: 2003-11-26

PRIOR FILING DATE: 2002-12-02

NUMBER OF SEQ ID NOS: 294

SEQ ID NO 195

LENGTH: 192
                                                                                                                                                                                                                                NAME/KBY: S'UTR
LOCATION: (1)...(4)

OTHER INPORMATION:
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
TATTUR: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
TITLE: that recognize Na+-channels
JOURNAL: TAXICON
1550END: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AACAAATACTGCAATAGGGAATGCACCATGGAAGCACCGAGGAGGTAATTACGGCTATTGC 120
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LOCATION: (1)..(192)
OTHER INFORMATION: Product= Sodium-channel modifier toxin
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Centruroides sculpturatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DATE: 2001-12-01
DATABASE ENTRY DATE:
RELEVANT RESIDUES: (5)..(262)
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LOCATION: (5)..(61)
OTHEN INPORMATION:
FEATURE:
NAME/KEY: 3'UTR
LOCATION: (266)..(320)
OTHER INPORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAGES: 1893-1898
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US-10-721-793-149
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LOCATION: (1)...(204)
OTHER INFORMATION: Product= Sodium-channel modifier toxin precursor
OTHER INFORMATION: In the mature peptide, the last Cys is amidated, and the last Gl
OTHER INFORMATION: and the last 2 basic aminoacids are cut
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antivenome to the
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                    1 AAAGACCCTTATCTCGTCGACAAGACGCGCTCCAAATACACTTGCTCGATATTGGGAGAA
                                                      61 AACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 45, Application US/10721793
; Sequence 45, Application US/10721793
; Publication No. US20050065331A1
; GENERAL INFORMATION:
; APPLICANT: Corona Villegae, Miguel
; APPLICANT: Corona Villegae, Ma Consuelo
; APPLICANT: Garcia Redriguez, Ma Consuelo
; APPLICANT: Garcia Redriguez, Ma Consuelo
; APPLICANT: Becerril Lujan, Baltazar
; TILE OF INVENTION: Vonom of Scorpione of the Genue Centruroidee
; TILE REFERRUE: 2099:00700011
; CURRENT FILING DATE: 2003-11-26
; CURRENT PLING DATE: 2003-11-26
; FRIOR PLING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 294
; SOFTHARE: Patentin version 3.1
; SEQ ID NO 45
; LENGTH: 258
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Best Local Similarity 87.0%; Pred. No. 2.8e-40;
Matches 167; Conservative 0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Centruroides exilicauda
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; LOCATION: (205)..(258)
; OTHER INFORMATION:
US-10-721-793-45
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Sequence 47, Application US/10721793

Publication No. US20050065331N1

GENERAL INFORMATION:
APPLICANT: Corona Villegas, Miguel
APPLICANT: Corona Villegas, Miguel
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Possani Descril Lujan, Baltazar
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Possani Postay, Lourival Domingos
APPLICANT: Neman of Scorpions of the Generation of Antivenoms to the
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
TITLE OF SCORPION: 1007-11-26

PRIOR TILING DATE: 2002-11-26

NUMBER OF SEQ ID NOS: 294

SEQ ID NOS: 294

SEQ ID NO 47-
                                                                                                                                                                     AUTHORS: Corona, M., Valdez-Cruz, N.A., Mexino, E., Zurita, M. & Possani L.D.
TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
TITLE: that recognize Na+-channels
JOURNAL. Toxicon
VOLUME: 19
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80.8%; Score 155.2; DB 9; Length 320;
Best Local Similarity 88.0%; Pred. No. 2.6e-41;
Matches 169; Conservative 0; Mismatches 23; Indels 0;
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Best Local Similarity 87.0%; Pred. No. 2.5e-40;
Matches 167; Conservative 0; Mismatches 25; Indels
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OTHER INFORMATION: Product Sodium-channel modifier toxin
PEATURE:
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ORGANISM: Centruroides exilicauda
                                                                                                                                                                                                                                                                                                                                       DATE: 2001-12-01
DATABASE ENTRY DATE:
RELEVANT RESIDUES: (5)..(262)
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                                                                                  NAMB/KBY: 819 peptide
LOCATION: (5)...(61)
OTHER INFORMATION:
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                     PAGES: 1893-1898
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us-lu-(al-(as)) Application US/10721793
; Sequence 19, Application US/10721793
; Publication No. US20050065331A1
; Publication No. US20050065331A1
; GENERAL INFORMATION:
; APPLICANT: Garcia Rodriguez, Ma Consuelo
; APPLICANT: Garcia Rodriguez, Ma Consuelo
; APPLICANT: Garcia Bationes, Georgina
; APPLICANT: Gurrola Briones, Georgina
; APPLICANT: Becerril Lujan, Baltearar
; APPLICANT: Becerril Lujan, Baltearar
; APPLICANT: Wenom of Scorpions of the Generation of Antivenome to the
; TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
; TITLE OF INVENTION NUMBER: US/10/721,793
; FILE REPRENCE: 2003-11-26
; FILE REPRENCE: 2002-11-02
; CURRENT PILLNG DATE: 2003-11-02
; RIOR APPLICATION NUMBER: US 60/430,067
; RIOR PILING DATE: 2002-12-02
; NUMBER OF SEC ID NOS: 294
; SOFTWARE PERCHIN Version 3.1
; SEQ ID NO 91
; LENGTH: 198
SEQ 1D NO 41
LENGTH: 254
TYPE: DNA
ORGANISM: Centruroides exilicanda
ORGANISM: Centruroides exilicanda
ORGANISM: Centruroides exilicanda
ORGANISM: Centruroides exilicanda
FRATURS:
FRATURS:
LOCATION: (1)...(204)
OTHER INFORMATION: DATE mature peptide, the last Cys is amidated, and the last Cys is FRATURE:
FRATURE:
FRATURE:
FRATURE:
FRATURE:
FRATURE:
FRATURE:
LOCATION: (205)...(254)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 78.3%; Score 150.4; DB 9; Length 254; Best Local Similarity 86.5%; Pred. No. 9.56-40; Matches 166; Conservative 0; Mismatches 26; Indels 0.
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; OTHER INFORMATION: Product= Sodium-channel modifier toxin
US-10-721-793-91
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ORGANISM: Centruroides noxius
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US-10-721-793-41
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                                                                                                        Sequence 43, Application US/10721793

Publication No. US20050065331A1
GENERAL INFORMATION
APPLICANT: Corona Villegas, Miguel
APPLICANT: Corona Villegas, Miguel
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: CONTROMENTION: Venom of Sorpions of the Genus Centruroides
CURRENT APPLICATION NUMBER: US/10/721,793
CURRENT APPLICATION NUMBER: US/610/067
PRIOR APPLICATION NUMBER: US 60/430,067
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin Version 3.1
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Fublication No. USZ050065331A1

GENERAL INPORMATION:
APPLICANT: Corona Villegas, Miguel
APPLICANT: Waldez Cruz, Norma Adriana
APPLICANT: Waldez Cruz, Norma Adriana
APPLICANT: Possani Postay, Louitval Domingos
TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
TITLE OF INVENTION: WINBER: US/10/721,793
CURRENT PLILIG DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 60/430,067
PRIOR PILICATION NUMBER: US 60/430,067
PRIOR PILICATION NUMBER: 202-12-02
PRIOR PILICATION NUMBER: 202-12-02
PRIOR PILICATION NUMBER: US 60/430,067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KGY: CDS
1 LOCATION: (1)..(192)
1 CTHEN INFORMATION: Product = Sodium-channel modifier toxin US-10-791-793-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Centruroides exilicauda
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US-10-721-793-41
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LENGTH: 192
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Antivenome to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 TATGCTTTTGGGTGCTATTGCGAAGGATTACCCGAAAGCGTACTGACCTCGCCCCTTTCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 AACAAATACTGCAATTCGGAATGC-----AAAGAGGTAGGTGCTGCTTACGGCTATTGC 117
                                                                            122 GAAAACAAAAACTGCGATATGGAATGCAAAGCGAAGAACCAAGGAGGTAGTTACGGCTAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 IGCTACGATTTGGGTGCTATTGCGAAGGATTGTCCGATAGTACACCGACTTGGCCCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAAGACGGTTATCTGGTGGACAAGACGGGCTGCAAATACACTTGCTGGATATTGGGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
                                                                                                                                                                                                                                                                                                   Sequence 111, Application US/10721793
Sequence 111, Application US/10721793
Sequence 111, Application US/10721793
Sequence 111, Application No. US20050065331A1
GENERAL INFORMATION
APPLICANT: Corona Villegas, Miguel
APPLICANT: Valdez Cruz, Norma Adriana
APPLICANT: Possani Postay, Lourival Domingos
APPLICANT: Possani Postay, Lourival Domingos
ITILE OF INVENTION: Vence of Scorpions of the Genus Centruroides
ITILE REPRENCE: 2099.0070001
ITILE REPRENCE: 2099.0070001
CURRENT APPLICATION NUMBER: US/10/721,793
CURRENT APPLICATION NUMBER: US 60/430,067
PRIOR APPLICATION NUMBER: US 60/430,067
SPRIOR PILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 294
SOFTHARE: Patentin Version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 66.0%; Score 126.8; DB 9; Length 189; Best Local Similarity 82.8%; Pred. No. 6.4e-32; Matches 159; Conservative 0; Mismatches 27; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (1)..(189)
; OTHER INFORMATION: Product= Sodium-channel modifier toxin
US-10-721-793-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search.completed: January 22, 2006, 01:12:50 Job time : 2178 8ec8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Centruroides elegans
                                                                                                                                                                              242 CCTAATAAAACATGC 256
                                                                                                                                                 178 TCTAATAAAGATGC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AATAAAAGATGC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 GATAAAACATGC 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 111
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1 Sequence 89, Application US/10721793

2 Sequence 89, Application US/10721793

2 Requence 89, Application US/10721793

3 Publication No. US20050065331A1

3 PAPLICANT: Corona Villegas, Miguel

3 APPLICANT: Carcia Rodriguez, Ma Consuelo

4 APPLICANT: Valdaz Cruz, Norma Adriana

3 APPLICANT: Valdaz Cruz, Norma Adriana

4 APPLICANT: Possani Postay, Lourival Domingos

5 APPLICANT: Becerril Lujan, Baltazar

5 APPLICANT: WINGRYION: Venom of Socryions of the Genus Centruroides

7 TITLE OP INVERTION: Venom of Socryions of the Genus Centruroides

7 TITLE OP INVERTION: Venom of Socryions of the Genus Centruroides

7 TITLE OP INVERTION: UNDER: US/10/721,793

7 CURRENT APLICATION NUMBER: US/10/721,793

7 CURRENT PILING DATE: 2002-11-26

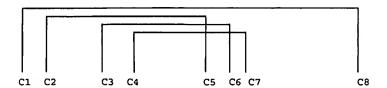
8 PRIOR PILING DATE: 2002-12-02

8 NUMBER OF SEQ ID NOS: 294

8 SOC ID NO 89

1 EMBRITH: 323

1 EMBRITH: 323
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LOCATION: (5)..(265)
OTHER INFORMATION: Froduct= Sodium-channel modifier toxin precursor
OTHER INFORMATION: In the mature peptide, the last Ser is smidsted, and the last Gly
OTHER INFORMATION: and the last basic aminoacid are cut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                    61 GABARCABABACTGCGATATGGBATGCBAGGGBAGACCAAGGAGGTGGTTACGGCTAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 AAGGAAGGTTATCTGGTGAAACACAAAGGCTGTTAATACAACTGCTTGATATTGGGA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAGGAAGGTTATCTGGTGAACAAAAGCACAGGCTGTAAATACAACTGCTTGATATTGGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 75.7%; Score 145.4; DB 9; Length 323; Best Local Similarity 87.7%; Pred. No. 4.9e-38; Matches 171; Conservative 0; Mismatches 21; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AAAGACGGTTATCTGGTGGACAA---GACGGGCTGCAAATACACTTGGTAATATGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAMES/RES: 5'UTR
LOCATION: (1)...(4)
OTHER INPORMATION:
FRATURE:
NAMES/RES: mat peptide
LOCATION: (62)...(3)
OTHER INPORMATION:
PROJUCT SOURCE SOGIUM-Channel modifier toxin
                                                                                                                                                                                                                                                      178 TCTAATAAAAGATGC 192
                                                                                                                                                                                                                                                                                181 CCTAATAAACATGC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPB: DNA
IGANISM: Centruroides noxius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (269)..(323)
OTHER INPORMATION:
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAMB/KGY: eig_peptide;
; LOCATION: (5)..(61)
; OTHER INFORMATION:
US-10-721-793-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAMB/KGY: 3'UTR
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Alignments:

Long-chain toxins specific for sodium channels:

A	В	C	
004	Cexl	KEGYLVSKSTGCKYEGFWLGKNEGCDKECKAPNQGGGYGYCHAFACWCENLPESTPTYPIPGKSC	53.8
008	Cex2	KEGYLVSKSTGCKYECTWLGKNEGCDKECKAPNOGGGYGYCHAFACWCENLPESTPTYPIPGKSC	53.8
036	Cex7	REGYLVSKSTGCKYEGFWLGKNEGCDKECKAPNOGGGYGYCHAFACWCENLPESTPTYPIPGKSC	52.3
028	Cex5	KDGYLVSKSTGÖKYEÖFWLGKNEGÖDKEÖKAPNOGGGYGYÖHAFAÖWÖENLPESTPTYPIPGKSÖ	55.3
104	Ce6	KEGYLVNKSTGCKYSCVLLGKNENCDKECKAKNOGGSYGYCYAFGCWCEGLPESTPTYPIPGKSC	60.0
	Ce6b	KDGYLVNKSTGCKYSCGKLGENEHCDKECKAKNQGGSYGYCYAFGCWCEGLPESTPTYPIPGKSC	63.0
	CsEv3b	KEGYLVNKSTGCKYGCLKLGENEGCDKECKAKNOGGSYGYCYAFACWCEGLPESTPTYPLPNKSC	63.0
	CsEv2a	KEGYLVNKSTGCKYGCLKLGENEGCDKECKAKNOGGSYGYCYAFACWCEGLPESTPTYPLPNKSCS	62.1
	CsEv2d	KEGYLVNKSTACKYGCLKLGENEGCDKECKAKNOGGSYGYCYAFACWCEGLPESTPTYPLPNKSCS	60.6
	CsEv2b	REGYLVNKSTGCKYGCLKLGENEGCDKECKAKNQGGSYGYCYAFACWCEGLPESTPTYPLPNKSCS	60.6
	CsEv2c	KEGYLVNKSTGCKYGCLKLGENEGCDKECKAENOGGSYGYCYAFACWCEGLPESTPTYPLPNKSCS	60.6
100	Ce5	KEGYLVNKSTGCKYGCLLLRKNEGCDKECKAKNQGGSYGYCYSFACWCEGLPESTPTYPLPNKSCSKK	57.3
	Cex4	KEGYLVNKSTGÖKYEGFWLGKNEFÖDKEGKAKNOGGSYGYGYSFAGWGEGLPESTSTYPLPNKSG	60.0
	Cex6	REGYLVNKSTGCKYECFWLGKNEFCDKECKAKNQGGSYGYCYSFACWCEGLPESTSTYPLPNKSC	58.4
	Cex3	KDGYLVNKSTGCKYECFWLGKNEFCDKECKAKNOGGSYGYCYSFACWCEGLPESTSTYPLPNKSC	61.5
	C115b	KEGYLVNKSTGCKYGCFWLGKNENCDKECKAKNQGGSYGYCYSFACWCEGLPDSTPTYPLPNKSCS	62.1
	C115c	KEGYLVNKSTGCKYGCFWLGKNENCDMECKAKNOGGSYGYCYSFACWCEGLPDSTPTYPLPNKSCS	62.1
140	CsEvld	KDGYLVNKSTGCKYDCFWLGKNEHCDLECKAKNQGGSYGYCYAFACWCEGLPESTPTYPLPNKSC	63.0
	CsEvic	KDGYLVKKSTGČKYDÖFWLGKNEHÖDLEČKAKNQGGSYGYÖYAFAÖWÖEGLPESTPTYPLPNKSÖ	63.0
	CsEvlb	KEGYLVKKSDGCKYDGFWLGKNEHCDTECKAKNQGGSYGYCYAFACWCEGLPESTPTYPLPNKSC	60.0
	CsEvle	KEGYLVKKSDGCKYDGFWLGENEGCDKECKAKNQGGSYGYCYAFACWCEGLPESTPYTPLPNKSC	60.0
	C118	KEGYLVKKSNGCKYECFKLGENEHCDTECKAPNQGGSYGYCDTFECWCEGLPESTPTWPLPNKSC	60.0
	Cnl0b	KEGYLVNKSTGCKYNCLILGENKNCDMECKAKNOGGSYGYCYGFGCYCEGLSDSTPTWPLPNKTCS	74.2
124	Cgl	KDGYLVKKSDGCKYGCMLKIGDAGCDKECKAPNQGGSYGYCYLLGCWCEGMPESTPTYPLPGKSC	52.3
128	Cglb	KDGYLVKESDGCKYGCMLKIGDAGCDKECKAPNQGGSYGYCYLLGCWCEGMPESTPTYPLPGKSC	52.3
136	Cg3	KDGYLVKKSDGCKYGCVMLVGDSGCDTECKAKNQGGKKCWCYAFGCWCTGMPDSTQVYPLPDKSC	49.2
016	Cex13	KDGYLVIIKTGCKYNCYILGKNKYCNSECKEVGAGYGYCYAFGCWCEGLPESIPTWPLPDKTCGTK	66.1
112	Ce7	KDGYLVN-KTGCKYNCWILGENKYCNSWCKEVGAGYGYCYAFGCYCEGLPESVLTWPLSDKTC	73.4
040	Cex8	KEGYLVNIYTGCKYSCWLLGENEYCIAECKEIGAGYGYCHGFGCWCEQFPENKPSYPYPEKSC	55.3
052	Cexll	KEGYPVNIYTGCKYSCWLLGENEYCIAECKEIGAGYGYCHGFGCWCEQFPENKPSYPYPEKSC	53.8
080	C117	KEGYLVNTYTGCKYICWKLGENKYCIDECKEIGAGYGYCYGFGCYCEGFPENKPTWPLPNKTC	67.6
044	Cex9	KDGYPVE-VTGCKKSCYKLGENKFCNRECKMKHRGGSYGYCYFFGCYCEGLAESTPTWPLPNKSC	75.0
048	Cex10	KDGYLVE-VTGCKKSCYKLGENKFCNRECKMKHRGGSYGYCYFFGCYCEGLAESTPTWPLPNKSC	76.5
152	CsEIa	KDGYLVE-KTGCKKTCYKLGENDFCNRECKWKHIGGSYGYCYGFGCYCEGLPDSTOTWPLPNKTC	79.6
	CsElx	KEGYLVD-VKGCKKNCWKLGDNDYCNRECKWKHIGGSYGYCYGFGCYCEGLPDSTQTWPLPNKTC	76.5
116	Ce13	KDGYLVD-KTGCKYTCWILGENKYCNRECTWKHRGGNYGYCYGFGCYCEGLSDSTPTWPLSNKRC	100.0
120	Cel3b	KDGYLVD-KTGCKYTCWILGENKYCNRECTWKHRGGNYGYCYCGGCYCEGLSDSTPTWPLPNKRC	95.3
056	C112b	KEGYLVNHSTGCKYECYKLGDNDYCLRECKQQYGKGAGGYCYAFGCWCTHLYEQAVVWPLPKKTCN	51.5
088	Cn4b	KEGYIVNSYTGCKYECLKLGDNDYCLRECKQQYGKGAGGYCYAFGCWCTHLYEQAVVWPLKNKTCN	51.5
	C114	KEGYIVNYHDGCKYECYKLGDNDYCLRECKLRYGKGAGGYCYAFGCWCTHLYEQAVVWPLPKKRCN	50.0
096	Ce3	KEGYIVNYHDGCKYECYKLGDNDYCLRECKLRYGKGAGGYCYAFGCWCTHLYEQAVVWPLPKKRCN	50.0
192	CsE3	KEGYIVNYHTGCKYECFKLGDNDYCLRECKLRHGKGSGGYCYAFGCWCTHLYEQAVVWPLPKKKCN	51.5
060	C113	KEGYIVNYYDGCKYACLKLGENDYCLRECKARYYKSAGGYCYAFACWCTHLYEQAVVWPLPNKTCY	48.4
076	C116	KEGYLVNMKTGCKYGCYELGDNGYCDRKCKAESGNYGYCYTVGCWCEGLPNSKPTWPLPGKSCS	62.1
188	CsE8	EKGYLVHEDTGCRYKCTFSGENSYCDKECKSQGGDSGICQSKACYCQGLPEDTKTWPLIGKLC	49.2
132	Cg2	KDGYLVNKSTGCKYSCIENINDSHCNEECISSIRKGSYGYCYKFYCYCIGMPDSTQVYPIPGKTCSTE	50.0
180	CsE9b	EDGYLFDKRKRCTLECIDKTCDKNCDRNCKNEGGSFGKCSYFACWCKGLPGITPISRTPGKTCKI-	35.8
184	CsE9	EDGYLFDKRKRCTLECIDMTGDKNCDRNCKKEGGSFGKCSYFACWCKGLPGITPISRTPGKTCKI-	35.8
	Cex12	NDGYLFDKRKRCTLECIDKTGDKNCDRNCKKEGGSFGKCSYSACWCKGLPGITPISRTPGKTC	35.3
	•		

Column A= SEQ. ID. No.

Column B= Clone name

Column C= amino acid sequences encoded by the DNAs

Column D= Is the percent of identity to SEQ.ID.NO:116, the amino acid sequence (mature peptide) encoded by the elected sequence SEQ.ID.NO:115.